

# BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (1935 letters)

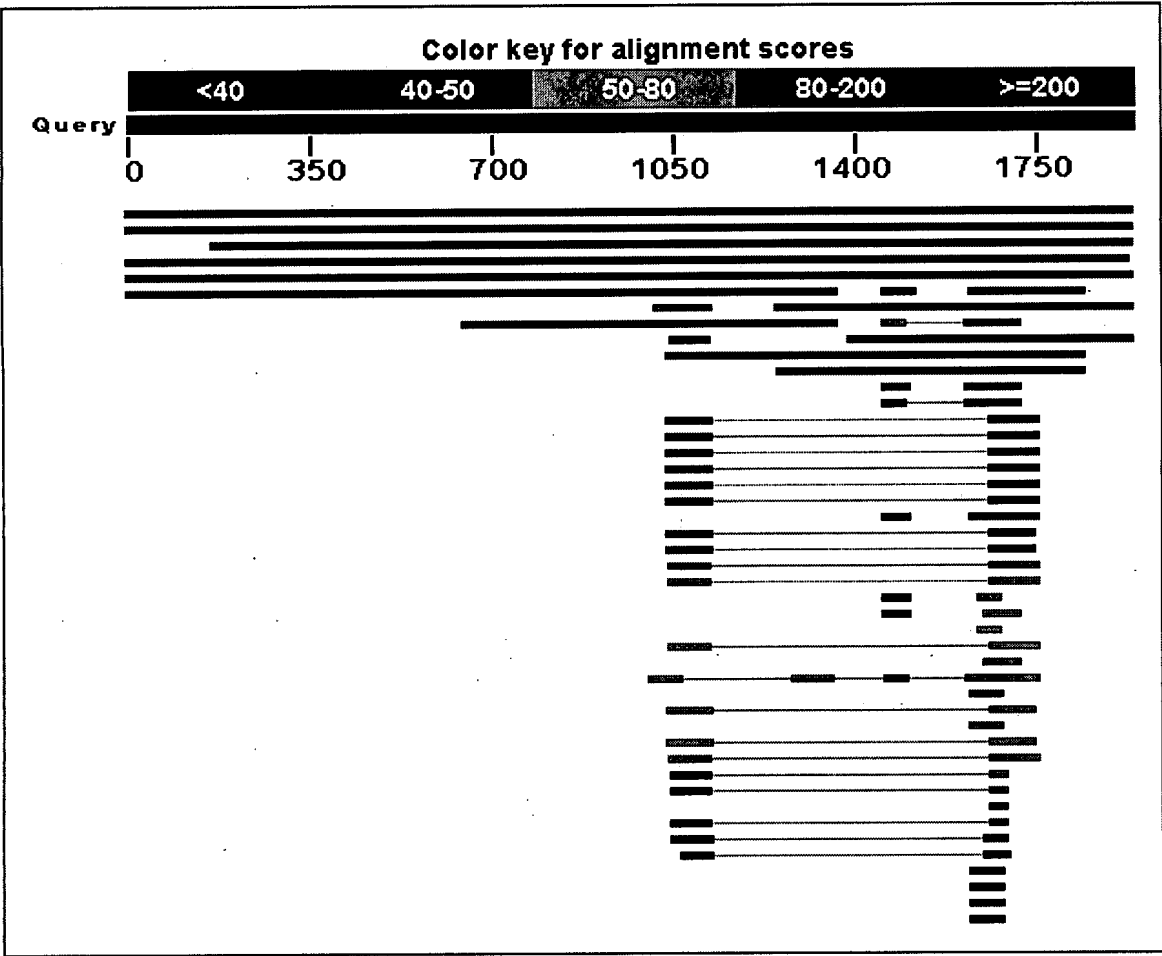
•  
•  
•

BLASTN 2.2.17 (Aug-26-2007)

RID: HHG6MUYH01N Database: "Geo" 283,711 sequences; 1,244,709,904 total letters

Query= Length=1935

## Distribution of 78 Blast Hits on the Query Sequence



Distance tree of results <sup>NEW</sup>

Sequences producing significant alignments:			Score (Bits)	E Value	
gi 34526552 dbj AK131104.1	Homo sapiens mRNA for FLJ00341 prote	3721	0.0	<b>UEG</b>	
gi 20521076 dbj AB011112.3	Homo sapiens mRNA for KIAA0540 prote	3715	0.0	<b>UEG</b>	
gi 38174270 gb BC060874.1	Homo sapiens neurobeachin-like 2, ...	3386	0.0	<b>UEG</b>	
gi 109483997 ref XM_236649.4	PREDICTED: Rattus norvegicus ne...	2267	0.0	<b>UEG</b>	
gi 51765227 ref XM_150243.4	PREDICTED: Mus musculus cDNA sequen	2040	0.0	<b>E</b>	
gi 27469592 gb BC042396.1	Mus musculus neurobeachin-like 2, ...	1413	0.0	<b>UEG</b>	
gi 23242934 gb BC035894.1	Homo sapiens neurobeachin-like 2, ...	1258	0.0	<b>UEG</b>	
gi 22902315 gb BC037746.1	Mus musculus neurobeachin-like 2, ...	873	0.0	<b>UEG</b>	
gi 30851326 gb BC052551.1	Mus musculus cDNA clone IMAGE:3469056	727	0.0	<b>UE</b>	
gi 37994643 gb BC060141.1	Mus musculus neurobeachin like 1, ...	212	3e-52	<b>UEG</b>	
gi 33417008 gb BC055813.1	Mus musculus neurobeachin like 1, ...	196	1e-47	<b>UEG</b>	
gi 26334212 dbj AK041108.1	Mus musculus adult male aorta and...	137	1e-29	<b>UEG</b>	
gi 39930598 ref NM_172882.2	Mus musculus WD repeat and FYVE ...	98.7	5e-18	<b>UEG</b>	
gi 26006236 dbj AB093277.1	Mus musculus mRNA for mKIAA0993 prot	98.7	5e-18	<b>UEG</b>	
gi 109499466 ref XM_223196.4	PREDICTED: Rattus norvegicus WD...	93.0	2e-16	<b>UEG</b>	
gi 117956398 ref NM_030695.2	Mus musculus LPS-responsive bei...	87.2	1e-14	<b>UEG</b>	
gi 26330689 dbj AK035483.1	Mus musculus adult male urinary b...	87.2	1e-14	<b>UEG</b>	
gi 26327124 dbj AK031216.1	Mus musculus 13 days embryo forel...	87.2	1e-14	<b>UEG</b>	
gi 10257400 gb AF188506.1 AF188506	Mus musculus LBA isoform beta	87.2	1e-14	<b>UEG</b>	
gi 10257404 gb AF188507.1 AF188507	Mus musculus LBA isoform gamm	87.2	1e-14	<b>UEG</b>	
gi 10180265 gb AF187731.1 AF187731	Mus musculus LBA (Lba) mRNA,	87.2	1e-14	<b>UEG</b>	
gi 10439364 dbj AK026491.1	Homo sapiens cDNA: FLJ22838 fis, ...	85.3	5e-14	<b>E</b>	
gi 109466822 ref XM_001066755.1	PREDICTED: Rattus norvegicus...	81.4	7e-13		
gi 109465018 ref XM_342271.3	PREDICTED: Rattus norvegicus LP...	81.4	7e-13		
gi 26335530 dbj AK043125.1	Mus musculus 7 days neonate cereb...	62.2	5e-07	<b>EG</b>	
gi 11863683 emb Y18276.1 MMU18276	Mus musculus mRNA for neurobea	62.2	5e-07	<b>UEG</b>	
gi 1556398 emb X96586.1 HSFAN	H.sapiens mRNA for FAN protein	62.2	5e-07	<b>UEG</b>	
gi 10440523 dbj AK024502.1	Homo sapiens mRNA for FLJ00111 prote	62.2	5e-07	<b>UEG</b>	
gi 31543296 ref NM_003580.2	Homo sapiens neutral sphingomyel...	62.2	5e-07	<b>UEG</b>	
gi 5305402 gb AF072372.1 AF072372	Mus musculus lysosomal traf...	62.2	5e-07	<b>UEG</b>	
gi 10047288 dbj AB046827.1	Homo sapiens mRNA for KIAA1607 prote	62.2	5e-07	<b>UEG</b>	
gi 113194865 gb AE014296.4	Drosophila melanogaster chromosome 3	58.4	6e-06	<b>E</b>	
gi 113193577 gb AE014298.4	Drosophila melanogaster chromosome X	58.4	6e-06	<b>E</b>	
gi 16716612 gb AF216648.2 AF216648	Homo sapiens LPS responsiv...	58.4	6e-06	<b>UEG</b>	
gi 15291502 gb AY051596.1	Drosophila melanogaster GH23814 full	58.4	6e-06	<b>UE</b>	
gi 1580780 gb M83822.1 HUMCDC4REL	Human beige-like protein (BGL)	58.4	6e-06	<b>UEG</b>	
gi 113194944 gb AE014134.5	Drosophila melanogaster chromosome 2	56.4	2e-05	<b>E</b>	
gi 109466684 ref XM_001059612.1	PREDICTED: Rattus norvegicus...	56.4	2e-05	<b>EG</b>	
gi 62422576 ref NM_015678.3	Homo sapiens neurobeachin (NBEA), m	52.6	4e-04	<b>UEG</b>	
gi 21434742 gb AF467288.1	Homo sapiens BCL8B protein (BCL8B) mR	52.6	4e-04	<b>UEG</b>	
gi 6808382 emb AL137748.1 HSM802363	Homo sapiens mRNA; cDNA D...	52.6	4e-04	<b>UEG</b>	
gi 10047152 dbj AB046764.1	Homo sapiens mRNA for KIAA1544 prote	52.6	4e-04	<b>UEG</b>	
gi 42566099 ref NM_115956.2	Arabidopsis thaliana beige/BEACH...	48.8	0.005	<b>UEG</b>	
gi 74199109 dbj AK155186.1	Mus musculus NOD-derived CD11c +v...	46.8	0.019	<b>UEG</b>	
gi 16758279 ref NM_053518.1	Rattus norvegicus lysosomal traf...	46.8	0.019	<b>UEG</b>	
gi 111955375 ref NM_010748.2	Mus musculus lysosomal trafficking	43.0	0.28	<b>UEG</b>	
gi 109503753 ref XM_001060720.1	PREDICTED: Rattus norvegicus...	43.0	0.28	<b>EG</b>	

<u>gi 26342211 dbj AK051786.1 </u>	Mus musculus 12 days embryo spina...	<u>43.0</u>	0.28	<b>EG</b>
<u>gi 1813541 gb U70015.1 MMU70015</u>	Mus musculus lysosomal traffi...	<u>43.0</u>	0.28	<b>UEG</b>
<u>gi 1675213 gb U52461.1 MMU52461</u>	Mus musculus beige (bg) mRNA, pa	<u>43.0</u>	0.28	<b>UEG</b>
<u>gi 31317271 ref NM_014991.3 </u>	Homo sapiens WD repeat and FYVE ...	<u>41.1</u>	1.0	<b>UEG</b>
<u>gi 23194376 gb AF538685.1 </u>	Homo sapiens ALFY mRNA, complete cds	<u>41.1</u>	1.0	<b>EG</b>
<u>gi 34367312 emb BX648153.1 HSM808300</u>	Homo sapiens mRNA; cDNA DKF	<u>41.1</u>	1.0	<b>UEG</b>
<u>gi 20521719 dbj AB023210.2 </u>	Homo sapiens mRNA for KIAA0993 prote	<u>41.1</u>	1.0	<b>UEG</b>

Database: "Geo"

Posted date: Sep 26, 2007 5:53 PM

Number of letters in database: 1,268,626,203

Number of sequences in database: 291,671

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 291671

Number of Hits to DB: 190948

Number of extensions: 15

Number of successful extensions: 13

Number of sequences better than 10: 8

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 13

Number of HSP's successfully gapped: 10

Length of query: 1935

Length of database: 1268626203

Length adjustment: 24

Effective length of query: 1911

Effective length of database: 1261626099

Effective search space: 2410967475189

Effective search space used: 2410967475189

A: 40

X1: 11 (21.1 bits)

X2: 31 (59.6 bits)

X3: 52 (100.0 bits)

S1: 15 (29.5 bits)

S2: 20 (39.1 bits)



# UniGene

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UGID:232080 UniGene Hs.437043 *Homo sapiens* NBEAL2

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## Neurobeachin-like 2 (NBEAL2)

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### SELECTED PROTEIN SIMILARITIES

Comparison of sequences in UniGene with selected protein reference sequences. The alignments can suggest function of a gene.

	Reference Protein	Species	Id(%)	Len(aa)
<a href="#">NP_055990.1</a>	neurobeachin-like 2	<i>H. sapiens</i>	100.0	2753
<a href="#">XP_236649.4</a>	PREDICTED: similar to neurobeachin-like 1	<i>R. norvegicus</i>	91.9	2744
<a href="#">XP_982666.1</a>	PREDICTED: neurobeachin-like 2	<i>M. musculus</i>	90.8	2749
<a href="#">XP_690862.1</a>	PREDICTED: similar to neurobeachin-like 1	<i>D. rerio</i>	74.3	842
<a href="#">NP_647876.1</a>	CG1332-PA	<i>D. melanogaster</i>	58.6	868
<a href="#">XP_421964.1</a>	PREDICTED: similar to FLJ00341 protein	<i>G. gallus</i>	57.1	2690
<a href="#">NP_009961.2</a>	beige protein homologue 1; Bph1p	<i>S. cerevisiae</i>	55.1	394
<a href="#">XP_324851.1</a>	hypothetical protein	<i>N. crassa</i>	48.3	547
<a href="#">NP_564728.2</a>	unknown protein	<i>A. thaliana</i>	47.5	736
<a href="#">NP_502422.1</a>	VT23B5.2	<i>C. elegans</i>	47.1	537
<a href="#">NP_001018801.1</a>	hypothetical protein SPBC3H7.16	<i>S. pombe</i>	45.7	576

### GENE EXPRESSION

Tissues and development stages from this gene's sequences survey gene expression. Links to other NCBI expression resources.

Expression Profile: View expression levels using UniGene's EST ProfileViewer

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Note: Highly represented (1.0 pct) in cDNA library dbEST:7892, EN0065.

GEO profiles: Gene expression profiles in the NCBI Gene Expression Omnibus database

### MAPPING POSITION

Genomic location specified by transcript mapping, radiation hybrid mapping, genetic mapping or cytogenetic mapping.

Chromosome:

3

Map position:

3p21.31

### SEQUENCES

Sequences representing this gene; mRNAs, ESTs, and gene predictions supported by transcribed

sequences.

### mRNA sequences (9)

<a href="#">AK131104.1</a>	Homo sapiens mRNA for FLJ00341 protein	<b>P</b>
<a href="#">AY358455.1</a>	Homo sapiens clone DNA35680 SQFE253 (UNQ253) mRNA, complete cds	<b>P</b>
<a href="#">BC060874.1</a>	Homo sapiens neurobeachin-like 2, mRNA (cDNA clone IMAGE:30348606), partial cds	<b>PA</b>
<a href="#">NM_015175.1</a>	Homo sapiens neurobeachin-like 2 (NBEAL2), mRNA	<b>PA</b>
<a href="#">AK074036.1</a>	Homo sapiens mRNA for FLJ00082 protein	<b>P</b>
<a href="#">AK092871.1</a>	Homo sapiens cDNA FLJ35552 fis, clone SPLEN2004346	<b>P</b>
<a href="#">BC029944.1</a>	Homo sapiens neurobeachin-like 2, mRNA (cDNA clone IMAGE:5189816)	<b>P</b>
<a href="#">BC035894.1</a>	Homo sapiens neurobeachin-like 2, mRNA (cDNA clone IMAGE:5219805), with apparent retained intron	<b>P</b>
<a href="#">AB011112.3</a>	Homo sapiens mRNA for KIAA0540 protein, partial cds	<b>P</b>

### EST sequences (10 of 384) [Show all sequences]

<a href="#">AA926792.1</a>	Clone IMAGE:1552328	3' read
<a href="#">AA927544.1</a>	Clone IMAGE:1552618	3' read <b>P</b>
<a href="#">AI146791.1</a>	Clone IMAGE:1706723	3' read <b>P</b>
<a href="#">CB049571.1</a>	Clone IMAGE:3271458	3' read <b>P</b>
<a href="#">CB049572.1</a>	Clone IMAGE:3271458	5' read <b>P</b>
<a href="#">CB051391.1</a>	Clone IMAGE:3289353	5' read <b>P</b>
<a href="#">AI147562.1</a>	Clone IMAGE:1555699	3' read <b>P</b>
<a href="#">CB070301.1</a>	Clone IMAGE:6554218	3' read
<a href="#">CB070359.1</a>	Clone IMAGE:6554218	5' read <b>P</b>
<a href="#">AI202100.1</a>	Clone IMAGE:1860078	3' read

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### Key to Symbols

**P** Has similarity to known **Pro**teins (after translation)  
**A** Contains a poly-**A**denylation signal  
**S** Sequence is a **S**uboptimal member of this cluster  
**M** Clone is putatively CDS-complete by **MGC** criteria



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Range: from  to  Features: ☒ CDD

☐ 1: [NP\\_055990](#). Reports neurobeachin-like...[gi:149944548]

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<a href="#">Comment</a>	<a href="#">Features</a>	<a href="#">Sequence</a>
LOCUS	NP_055990	2754 aa linear PRI 29-JUN-2007
DEFINITION	neurobeachin-like 2 [Homo sapiens].	
ACCESSION	NP_055990 XP_291064 XP_946304	
VERSION	NP_055990.1 GI:149944548	
DBSOURCE	REFSEQ: accession <a href="#">NM_015175.1</a>	
KEYWORDS	.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (residues 1 to 2754)	
AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I., Godowski,P. and Gray,A.	
TITLE	The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment	
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)	
PUBMED	<a href="#">12975309</a>	
REMARK	Erratum:[Genome Res. 2003 Dec;13(12):2759]	
COMMENT	VALIDATED REFSEQ: This record has undergone preliminary review of the sequence, but has not yet been subject to final review. The reference sequence was derived from <a href="#">CR988681.1</a> , <a href="#">AK131104.1</a> , <a href="#">AB011112.3</a> and <a href="#">BC060874.1</a> . On or before Jun 29, 2007 this sequence version replaced gi:113414493, gi:113415050.	
FEATURES	Location/Qualifiers	
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Protein	1..2754 /product="neurobeachin-like 2" /calculated_mol_wt=302387	
Region	1918..2003 /region_name="Neurobeachin" /note="Neurobeachin Pleckstrin homology-like domain. This domain is found in the large multi-domain eukaryotic protein Nerubeachin, N-terminal to the BEACH domain; cd01201" /db_xref="CDD:29850"	

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1974..1978,1987..1993,1997..2001)  
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Site order(1977,1979..1981,1983,1989,1991,1997,1999)  
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/note="Beige/BEACH domain; pfam02138"  
/db\_xref="CDD:65883"

Region 2464..2713  
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/note="WD40 domain, found in a number of eukaryotic  
proteins that cover a wide variety of functions including  
adaptor/regulatory modules in signal transduction,  
pre-mRNA processing and cytoskeleton assembly; typically  
contains a GH dipeptide 11-24 residues from; cd00200"  
/db\_xref="CDD:29257"

Site order(2476,2481,2487..2488,2500..2501,2519,2523,  
2529..2530,2551..2552,2569,2574,2580..2581,2596,2615,2621,  
2634..2635,2646..2647,2662,2666,2672..2673,2685..2686,  
2703,2708)  
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# ORIGIN

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181 saffqeslqn adhlppilll rlihlfcavl aggkengqma vsdgsvkgll svvrgwsrgp
241 apdpclvpla lealvgavhv lhasrapprg pelrallesy fhvlnadwpa glssgpeeal
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361 trllltepdvq kvldqdt dai avhvrvrltc imsdsp sake vfkerigyph lqevlqshgp
421 pthrlilqell nmavegdhsm cppppirneq pvlvlaqwl p slptaerlrf laqrlrlwld
481 scpasratcv qaglvgcille tlstglalea rcqeqlall galgrvsirp melrhllrpr
541 pgldsepqga eagkarhaga virtlsgmar hqgparalry fdltpsmagi mvpppvqrwpq
601 pgftfhawlc lhpmdtapt aptrplqrkq lysfftssgs gfeafftaag tlvvavctrk
661 eyltmslpev sfadsawhcv aivhvpgrrp fsqnlvhvyk dghlvktapl rcpslsepfs
721 sccigsagyr ttttttglpt ppvpatlayt hpaltersqsv pastglgwgs glvaplgqgs
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901 rvaaqpkeae agpaethdlv gpelstghnt qglvplpgks seermernav aafllmlrnf
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```

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1981 fnlrrsalel ffidqanyfl nfpckvgttp vsspsqtrp qpgpipphqtq vrnqvyswll  
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2221 yfpdflenqn gfdlgclqlt nekvgdvvlp pwasspedfi qqhrqalese yvsahlhewi  
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2341 phptrlsae aahrlarldt nspsifqhld elkaffaevv sdgvplvlal vphrqphsfi  
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2701 hvlvgledgk livvvagqps evrssqfark lwrssrrisq vssgeteynp tear

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